

ENTERED



PCT10

RAW SEQUENCE LISTING

DATE: 08/13/2002

PATENT APPLICATION: US/10/069,427

TIME: 15:46:13

Input Set : A:\BB1395 USPCT Corrected Seq.txt

Output Set: N:\CRF3\08132002\J069427.raw

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3 <110> APPLICANT: Famodu, Omolayo O.
4 Kinney, Anthony J.
7 <120> TITLE OF INVENTION: Genes Encoding Sterol Delta-15 Reductase in Plants
9 <130> FILE REFERENCE: BB1395 PCT
11 <140> CURRENT APPLICATION NUMBER: 10/069,427
C--> 12 <141> CURRENT FILING DATE: 2002-07-16
14 <150> PRIOR APPLICATION NUMBER: 60/156,820
15 <151> PRIOR FILING DATE: 1999-09-30
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: Microsoft Office 95
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 427
23 <212> TYPE: DNA
24 <213> ORGANISM: Glycine max
26 <220> FEATURE:
27 <221> NAME/KEY: unsure
28 <222> LOCATION: (360)
29 <223> OTHER INFORMATION: n=a,c,g or t
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32 gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac tccatcttgg 60
33 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 120
34 cctggaaaac ttgttcttgg cgttgcaacta ctcgatggaa ctcgtctaca ctattgctgc 180
35 aatgggtctgc tctcgttctt tctgttggtt gcacttctcg ggatcgggtgc caagatgggt 240
36 tttgtgtctc ccaactgccat atcaaacaga ggacttgagc tgctgtccac aacttttgcc 300
W--> 37 ttcagttttc ttgtaaccct gatattgcat ttttcggggt gcaagtcaca aagtaaagg 360
38 tcatcactaa agcctcatct cagtgggaac ctgatacacg attggtggtt tgggaataca 420
39 actaaaaa 427
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 126
44 <212> TYPE: PRT
45 <213> ORGANISM: Glycine max
47 <400> SEQUENCE: 2
48 Leu Gln Ala Leu Thr Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly
49 1 5 10 15
51 Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
52 20 25 30
54 Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
55 35 40 45
57 Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
58 50 55 60
60 Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
61 65 70 75 80
63 Glu Leu Leu Ser Thr Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile

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64          85          90          95
66 Leu His Phe Ser Gly Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys
67          100          105          110
69 Pro His Leu Ser Gly Asn Leu Ile His Asp Trp Trp Phe Gly
70          115          120          125
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 1631
75 <212> TYPE: DNA
76 <213> ORGANISM: Glycine max
78 <400> SEQUENCE: 3
79 ccgcgttgga atttgcccat ctaaaacctc aatctttttac tgaaaagtct caactttgaa 60
80 ctactcgaag gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac 120
81 tccatcttgg aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg 180
82 atccattctc cctggaaaac ttgttcctgg cgttgcaacta ctcgatggaa ctcgctctaca 240
83 ctattgctgc aatgggtctgc tctcgtttct tctgttggtt gcacttctcg ggatcggtgc 300
84 caagatgggt tttgtgtctc ccaactgccat atcagacaga ggacttgagc tgctgtccac 360
85 aacttttgcc ttcagttttc ttgtaaccct gatattgcat ttttcgggtt gcaagtcaca 420
86 aagtaaaggt tcatcactaa agcctcatct cagtggaaac ctgatacacg attggtgggt 480
87 tggatataca ctaaatccac agttcatggg tatcgacctc aaatttttct ttgttagagc 540
88 tggaatgatg ggatggctac ttatcaattt atctattctt atgaagagca ttcaagatgg 600
89 tactttgagc cagtcaatga ttctctacca gctattctgt gcactataca tcctggacta 660
90 ttttgtacat gaagagtaca tgacatccac ctgggacata attgcagaga gactgggctt 720
91 catgttggtc tttggagatt tagtgtggat tcctttctct ttcagcatac agggatgggt 780
92 gctcttgatg aacagtgtgg agttaacacc agctgccatt gtagctaatt gctttgtgtt 840
93 cctgattgga tacatggtat ttcgaggagc aaacaagcaa aagcatgtgt tcaaaaagaa 900
94 tccaaaggct cctatctggg gtaagcctcc aaaagtcatt ggtggaaagc tacttgcttc 960
95 tgggtattgg ggtattgcta gacactgtaa ttacctaggg gatttgatgc ttgctctctc 1020
96 ctttagctta ccatgtggga taagttcacc aattccatac ttctatccaa tttatcttct 1080
97 tattctgtta atctggagag agagaaggga tgaagctcgt tgcgccgaga agtatagaga 1140
98 gatatgggac gagtatcgta aacttgttcc atggagaata ttgccttacg tttattagga 1200
99 tgaaaaaaa aagggttcca ccatgaattc ttcattctgc cgatgttatt aagcacttcg 1260
100 atgtaaattg gttcttggtc ttgtggtttc aatcttggat cttttcttat tgagccatgt 1320
101 agctgcagga gagtggttgc agggatttat ctaccatct atatttgtgt atcattatgc 1380
102 tgcagcctgc aggccttcat tttcaatgg ccaactcttt ttgacttggt ctatttggtt 1440
103 ttagatgaga atttcatggt caaagctcct aggccttaaaa aaacagtgtc atgttctatg 1500
104 ggaagtgcag gaagcaattc ggggactgca ggaagcaatt gcctttacat tgatatgctc 1560
105 aatggtactt taggcccttt aatgttcttg cttttcattt gtgagttatt attggcccca 1620
106 tttcatttgc a 1631
109 <210> SEQ ID NO: 4
110 <211> LENGTH: 374
111 <212> TYPE: PRT
112 <213> ORGANISM: Glycine max
114 <400> SEQUENCE: 4
115 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
116 1 5 10 15
118 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
119 20 25 30
121 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
122 35 40 45

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124 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
125      50                      55                      60
127 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
128 65                      70                      75                      80
130 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
131      85                      90                      95
133 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
134      100                     105                     110
136 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
137      115                     120                     125
139 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
140      130                     135                     140
142 Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
143 145                      150                      155                      160
145 Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
146      165                     170                     175
148 Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
149      180                     185                     190
151 Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
152      195                     200                     205
154 Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
155      210                     215                     220
157 Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
158 225                      230                      235                      240
160 Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
161      245                      250                      255
163 Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
164      260                      265                      270
166 Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
167      275                      280                      285
169 Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
170      290                      295                      300
172 Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
173 305                      310                      315                      320
175 Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
176      325                      330                      335
178 Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
179      340                      345                      350
181 Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
182      355                      360                      365
184 Ile Leu Pro Tyr Val Tyr
185      370
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 667
190 <212> TYPE: DNA
191 <213> ORGANISM: Zea mays
193 <400> SEQUENCE: 5
194 ccacgcgtcc ggaagaacaa agtagagctg tcccttttgt ctggtctagc taacttatgc 60
195 atctttctta ttggctacct agtggtccga ggagctaaca agcaaaaaca tgtgttcaag 120

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196 aaggacccca aagctcctat atggggaaaa cctcccaaag ttgtcggggg aaagctacta 180
197 gcatctggtt actggggcat cgcaaggcac tgcaattatc tcggagacct gctgctagca 240
198 ctttcgttca gcttgccctg tggagtgagt tccgtggtcc catacttcta cccacgtac 300
199 ctgctcattc tactggtctt gagggaaaag cgcgatgagg cgagggtgctc gcagaagtac 360
200 agggagatct gggcagagta ctgcaagctc gtgccgtgga ggatcctgcc ttatgtgtac 420
201 tgaagagacg gtagaaacca aggcagctca tggccctggg ccagctgtaa accttatttt 480
202 gtttgccctt aaccagttgg tgaatgttga tgtagcactc ggtaaactgt gaccgtgcaa 540
203 acttttggtt ttgttggtcc atacatgttt ggaatcgtga atcagaccgc ctcacttggg 600
204 ggcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660
205 aaaaaag 667

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208 <210> SEQ ID NO: 6

209 <211> LENGTH: 140

210 <212> TYPE: PRT

211 <213> ORGANISM: Zea mays

213 <400> SEQUENCE: 6

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214 Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
215   1           5           10          15
217 Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
218           20          25          30
220 Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
221           35          40          45
223 Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
224           50          55          60
226 Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
227 65           70          75          80
229 Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
230           85          90          95
232 Tyr Pro Thr Tyr Leu Leu Ile Leu Leu Val Leu Arg Glu Arg Arg Asp
233           100         105         110
235 Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
236           115         120         125
238 Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
239           130         135         140

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242 <210> SEQ ID NO: 7

243 <211> LENGTH: 1364

244 <212> TYPE: DNA

245 <213> ORGANISM: Glycine max

247 <400> SEQUENCE: 7

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248 ttcggcacga gtaaacctc aatcttttac tgaagagtct caactttgaa ctcactcgaa 60
249 gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac tccatcttgg 120
250 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 180
251 cctggaaaac ttgttcctgg cgttgacta ctcgatggaa ctcgcttaca ctattgctgc 240
252 aatggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcggtgc caagatgggt 300
253 tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac aacttttgcc 360
254 ttcagttttc ttgtaacctt gatattgcat tttccggtt gcaagtcaca aagtaaagg 420
255 tcatcactaa agcctcatct cagtggaaac ctgatacacg attggtgggt tggatatacaa 480
256 ctaaatecac agttcatggg tatcgacctc aaagctggaa tgatgggatg gctacttctc 540
257 aatttatcta ttcttatgaa gagcattcaa gatggtactt tgagccagtc aatgattctc 600
258 taccagctat tctgtgcact atacatcctg gactattttg tacatgaaga gtacatgaca 660

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259 tccacctggg acataattgc agagagactg ggcttcatgt tggctcttgg agatttagtg 720
260 tggattcctt tctctttcag catacagga tgggtggctct tgatgaacag tgtggagtta 780
261 acaccagctg ccattgtagc taattgcttt gtgttcctga ttggatacat ggtatttcga 840
262 ggagcaaaca agcaaaagca tgtgttcaaa aagaatccaa aggctcctat ctggggtaag 900
263 cctccaaaag tcattggtgg aaagctactt gcttctgggtt attgggggtat tgctagacac 960
264 tgtaattacc taggggattt gatgcttget ctctccttta gcttaccatg tgggataagt 1020
265 tcaccaattc catacttcta tccaatttat cttcttattc tgtaaatctg gagagagaga 1080
266 acggatgaag ctggttgccg cgagaagtat agagagatat gggccgagta tcgtaaacctt 1140
267 gttccatgga gaattattgcc ttacgtttat taggatgaaa aaaaaaaggg cttcaccatg 1200
268 aattcttcat cttgccgatg ttattaagca cttcgatgta aattggttct tgttcttgtg 1260
269 gtttcaatct tggatctttt cttattgagc catgtagctg caggagagtg tttcgaggga 1320
270 tttatcttac catctatatt tgtgtaaaaa aaaaaaaaaa aaaa 1364

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273 <210> SEQ ID NO: 8

274 <211> LENGTH: 369

275 <212> TYPE: PRT

276 <213> ORGANISM: Glycine max

278 <400> SEQUENCE: 8

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279 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
280 1 5 10 15
282 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
283 20 25 30
285 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
286 35 40 45
288 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
289 50 55 60
291 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
292 65 70 75 80
294 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
295 85 90 95
297 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
298 100 105 110
300 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
301 115 120 125
303 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
304 130 135 140
306 Met Gly Ile Asp Leu Lys Ala Gly Met Met Gly Trp Leu Leu Ile Asn
307 145 150 155 160
309 Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly Thr Leu Ser Gln Ser
310 165 170 175
312 Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe
313 180 185 190
315 Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg
316 195 200 205
318 Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser
319 210 215 220
321 Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr
322 225 230 235 240
324 Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met
325 245 250 255

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/13/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 360

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300